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#85K  
8/11/00

1642

RAW SEQUENCE LISTING DATE: 07/24/2000  
 PATENT APPLICATION: US/09/434,708 TIME: 16:52:46

Input Set : A:\B8017159.txt  
 Output Set: N:\CRF3\07242000\I434708.raw

4 <110> APPLICANT: Borriello, Francescopaolo  
 5 Band, Hamid  
 7 <120> TITLE OF INVENTION: Characterization of a novel gene Cbl-SL  
 10 <130> FILE REFERENCE: B0801/7159/ERP  
 12 <140> CURRENT APPLICATION NUMBER: 09/434,708  
 13 <141> CURRENT FILING DATE: 1999-11-05  
 15 <150> PRIOR APPLICATION NUMBER: U.S. 60/107,470  
 16 <151> PRIOR FILING DATE: 1998-11-06  
 18 <160> NUMBER OF SEQ ID NOS: 10  
 20 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1547  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo Sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (13)...(1434)  
 31 <400> SEQUENCE: 1  
 32 cgcgaggctc cc atg gct ctg gcg gtg gcc ccg tgg ggg cga cag tgg gaa 51  
 33 Met Ala Leu Ala Val Ala Pro Trp Gly Arg Gln Trp Glu  
 34 1 5 10  
 36 gag gcc cgc gcc ctg ggc cgg gca gtc agg atg ctg cag cgc cta gaa 99  
 37 Glu Ala Arg Ala Leu Gly Arg Ala Val Arg Met Leu Gln Arg Leu Glu  
 38 15 20 25  
 40 gag caa tgc gtc gac ccc cgg ctg tcc gtg agt ccc cct tcg ctg cgg 147  
 41 Glu Gln Cys Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg  
 42 30 35 40 45  
 44 gac ctg ctg ccc cgc aca gcg cag ctg ctt cga gag gtg gcc cat tct 195  
 45 Asp Leu Leu Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser  
 46 50 55 60  
 48 cgg cgg gcg gcc gga ggc ggc ccc ggg ggt ccc ggc ggc tct ggg 243  
 49 Arg Arg Ala Ala Gly Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly  
 50 65 70 75  
 52 gac ttt cta ctc atc tac ctg gcc aat ctg gag gcc aag agc agg cag 291  
 53 Asp Phe Leu Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln  
 54 80 85 90  
 56 gtg gcc gcg ctg ctg ccc cgg ggc cga agg agt gcc aac gac gag 339  
 57 Val Ala Ala Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu  
 58 95 100 105  
 60 ctc ttc cgg ggc tcc aga ctc agg cga cag ctg gcc aag ctg gcc 387  
 61 Leu Phe Arg Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala  
 62 110 115 120 125  
 64 atc atc ttc agc cac atg cac gca gag ctg cac gca ctc ttc ccc ggg 435  
 65 Ile Ile Phe Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly  
 66 130 135 140  
 68 gca aag tac tgt gga cac atg tac cag ctc acc aag gcc ccc gcc cac 483  
 69 Ala Lys Tyr Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His

05  
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Input Set : A:\B8017159.txt  
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70	145	150	155	
72	acc ttc tgg agg gaa agt tgc gga gcc cgg tgt gtg ctg ccc tgg gct			531
73	Thr Phe Trp Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala			
74	160	165	170	
76	gag ttt gag tcc ctc ctg ggc acc tgc cac cct gtg gaa cca ggc tgc			579
77	Glu Phe Glu Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys			
78	175	180	185	
80	aca gcc ctg gcc ttg cgc acc acc att gac ctc acc tgc agc ggg cac			627
81	Thr Ala Leu Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His			
82	190	195	200	205
84	gtg tcc atc ttc gag ttc gac gtc ttc acc agg ctc ttt cag cca tgg			675
85	Val Ser Ile Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp			
86	210	215	220	
88	cca aca ctc ctc aag aac tgg cag ctc ctg gca gtc aac cac cca ggc			723
89	Pro Thr Leu Leu Lys Asn Trp Gln Leu Leu Ala Val Asn His Pro Gly			
90	225	230	235	
92	tac atg gcc ttc ctc acc tat gat gag gtc caa gag cgt ctg cag gcc			771
93	Tyr Met Ala Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala			
94	240	245	250	
96	tgc agg gac aag cca ggc agt tac atc ttc cgg ccc agc tgt act cgc			819
97	Cys Arg Asp Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg			
98	255	260	265	
100	ctg ggg cag tgg gcc atc ggc tat gtg agc tca gat ggc agc atc ctg			867
101	Leu Gly Gln Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu			
102	270	275	280	285
104	cag acc atc cct gcc aac aaa ccc ctg tcc cag gtg ctc ctg gag gga			915
105	Gln Thr Ile Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Glu Gly			
106	290	295	300	
108	cag aag gac ggc ttc tac ctc tac cca gat gga aag acc cac aac cca			963
109	Gln Lys Asp Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro			
110	305	310	315	
112	gac ctg act gag ctc ggc cag gca gaa ccc cag cag cgc atc cac gtg			1011
113	Asp Leu Thr Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg Ile His Val			
114	320	325	330	
116	tca gag gag cag ctg cag ctc tac tgg gcc atg gac tcc aca ttt gag			1059
117	Ser Glu Glu Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr Phe Glu			
118	335	340	345	
120	ctc tgc aag atc tgt gct gag agc aac aag gat gtg aag att gag cgc			1107
121	Leu Cys Lys Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro			
122	350	355	360	365
124	tgc ggg cac ctg ctc tgc agc tgc tgc ctg gct gcc tgg cag cac tgc			1155
125	Cys Gly His Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp Gln His Ser			
126	370	375	380	
128	gac agc cag acc tgc ccc ttc tgc cgc tgc gag atc aag ggc tgg gag			1203
129	Asp Ser Gln Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Trp Glu			
130	385	390	395	
132	gcc gtg agt atc tac cag ttc cac ggt cag gct act gct gag gac tca			
133	Ala Val Ser Ile Tyr Gln Phe His Gly Gln Ala Thr Ala Glu Asp Ser			
134	400	405	410	

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136 ggg aac agc agt gac cag gaa ggc agg gag ttg gag ctg ggg cag gtg 1299  
 137 Gly Asn Ser Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val  
 138 415 420 425  
 140 ccc ctt tcg gct cct cca ttg ccc cca cgg cca gat ctg ccc ccc agg 1347  
 141 Pro Leu Ser Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg  
 142 430 435 440 445  
 144 aag ccc aga aat gcc cag ccg aaa gtg aga ctc cta aag ggg aac tcc 1395  
 145 Lys Pro Arg Asn Ala Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser  
 146 450 455 460  
 148 cct cca gct gcg ctg gga ccc cag gac cct gcc ccg gcc tgaaggccag 1444  
 149 Pro Pro Ala Ala Leu Gly Pro Gln Asp Pro Ala Pro Ala  
 150 465 470  
 152 ggcacccaga tggctgctc aaggagccc caaggctgg aagggggttg tgaaaccgaa 1504  
 153 ataaactgcc aaggctggtc tgtcaaaaaa aaaaaaaaaa aaa 1547  
 155 <210> SEQ ID NO: 2  
 156 <211> LENGTH: 474  
 157 <212> TYPE: PRT  
 158 <213> ORGANISM: Homo Sapiens  
 160 <400> SEQUENCE: 2  
 161 Met Ala Leu Ala Val Ala Pro Trp Gly Arg Gln Trp Glu Glu Ala Arg  
 162 1 5 10 15  
 163 Ala Leu Gly Arg Ala Val Arg Met Leu Gln Arg Leu Glu Glu Gln Cys  
 164 20 25 30  
 165 Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg Asp Leu Leu  
 166 35 40 45  
 167 Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser Arg Arg Ala  
 168 50 55 60  
 169 Ala Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly Asp Phe Leu  
 170 65 70 75 80  
 171 Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln Val Ala Ala  
 172 85 90 95  
 173 Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu Leu Phe Arg  
 174 100 105 110  
 175 Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala Ile Ile Phe  
 176 115 120 125  
 177 Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly Ala Lys Tyr  
 178 130 135 140  
 179 Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His Thr Phe Trp  
 180 145 150 155 160  
 181 Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala Glu Phe Glu  
 182 165 170 175  
 183 Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys Thr Ala Leu  
 184 180 185 190  
 185 Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His Val Ser Ile  
 186 195 200 205  
 187 Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp Pro Thr Leu  
 188 210 215 220  
 189 Leu Lys Asn Trp Gln Leu Ala Val Asn His Pro Gly Tyr Met Ala  
 190 225 230 235 240

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Input Set : A:\B8017159.txt  
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191 Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala Cys Arg Asp  
 192 245 250 255  
 193 Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg Leu Gly Gln  
 194 260 265 270  
 195 Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu Gln Thr Ile  
 196 275 280 285  
 197 Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Glu Gly Gln Lys Asp  
 198 290 295 300  
 199 Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro Asp Leu Thr  
 200 305 310 315 320  
 201 Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg Ile His Val Ser Glu Glu  
 202 325 330 335  
 203 Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr Phe Glu Leu Cys Lys  
 204 340 345 350  
 205 Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro Cys Gly His  
 206 355 360 365  
 207 Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp Gln His Ser Asp Ser Gln  
 208 370 375 380  
 209 Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Trp Glu Ala Val Ser  
 210 385 390 395 400  
 211 Ile Tyr Gln Phe His Gly Gln Ala Thr Ala Glu Asp Ser Gly Asn Ser  
 212 405 410 415  
 213 Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val Pro Leu Ser  
 214 420 425 430  
 215 Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg Lys Pro Arg  
 216 435 440 445  
 217 Asn Ala Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser Pro Pro Ala  
 218 450 455 460  
 219 Ala Leu Gly Pro Gln Asp Pro Ala Pro Ala  
 220 465 470  
 222 <210> SEQ ID NO: 3  
 223 <211> LENGTH: 1422  
 224 <212> TYPE: DNA  
 225 <213> ORGANISM: Homo Sapiens  
 227 <400> SEQUENCE: 3  
 228 atggctctgg cgggtggccc gtgggggcga cagtggaaag aggccgcgc cctggggccgg 60  
 229 gcagtcaggat tgctgcagcg cttagaagag caatgcgtcg acccccggtc gtccgtgagt 120  
 230 ccccccgcg tgcgggacct gtcgccccgc acagcgcagc tgcttcgaga ggtggcccat 180  
 231 ttcgcggcgg cggccgcggc aggcggcccc ggggtcccg gccgcgttcgg ggactttcta 240  
 232 ctcatctacc tggccaaatct ggaggcacaag agcaggcagg tggccgcgtc gtcgcctccc 300  
 233 cggggccgaa ggagtgccaa cgcacgagtc ttccggcgq gtcgcagact caggcgcacag 360  
 234 ctggccaagg tggccatcat cttcagccac atgcacgcag agctgcacgc actttcccc 420  
 235 gggggaaagt actgtggaca catgtaccag ctcaccaagg ccccccgcaca caccctctgg 480  
 236 agggaaagt gcgagcccg gtgtgtgtcgc ccctgggcgt agtttgagtc ctcctgggc 540  
 237 acctggcacc ctgtggaaacc aggtgcaca gcccctggcct tgcgcacccat cattgacctc 600  
 238 acctgcagcg ggcaacgtgtc catttcgag ttgcacgtct tcaccaggtc ctttcagcca 660  
 239 tggccaaacac tcctcaagaa ctggcagctc ctggcagtca accacccagg ctacatggcc 720  
 240 ttccctcacct atgatgaggt ccaagagcgt ctgcaggcct gcagggacaa gccaggcagt 780  
 241 tacatcttcc ggcggcgtg tactcgcctg gggcgtggg ccacatggccta tgtgagctca 840

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PATENT APPLICATION: US/09/434,708

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Input Set : A:\B8017159.txt  
Output Set: N:\CRF3\07242000\I434708.raw

242	gatggcagca tcctgcagac catccctgcc	aacaaacccc tggcccaagg tgcctggag	900
243	ggacagaagg acggcttcta cctctaccca	gatggaaaga cccacaaccc agacctgact	960
244	gagtcggcc aggacgaaacc ccacgcgc	atccacgtgt cagaggagca gtcacgtctc	1020
245	tactggccca tggactccac atttgcgtc	tgcaagatct tgctggagag caacaaggat	1080
246	gtgaaggattt agccgtcg	gacatgtc tgcacgtctc gctggctgc ctggcagcac	1140
247	tcggcagcc agacctgcc	tttgcgtccgc tgcgagatca agggctggga ggccgtgagt	1200
248	atcttaccatg tccacggtca ggctactgt	gaggactca gaaacagcag tgaccaggaa	1260
249	ggcaggagt tggagctgg gcacgtgccc	cttgcgtccctc ctcattgtcc cccacggcca	1320
250	gatctcccccc ccaggaaagc	cagaatgcc cagccgaaag tgagactctt aaaggaaac	1380
251	tccctccca gtcgtcg	gaccaggac cttgcggcc	1422
253	<210> SEQ ID NO: 4		
254	<211> LENGTH: 462		
255	<212> TYPE: DNA		
256	<213> ORGANISM: Homo Sapiens		
258	<220> FEATURE:		
259	<221> NAME/KEY: unsure		
260	<222> LOCATION: (100)...(100)		
261	<223> OTHER INFORMATION: unknown		
263	<221> NAME/KEY: unsure		
264	<222> LOCATION: (103)...(103)		
265	<223> OTHER INFORMATION: unknown		
267	<221> NAME/KEY: unsure		
268	<222> LOCATION: (105)...(105)		
269	<223> OTHER INFORMATION: unknown		
271	<221> NAME/KEY: unsure		
272	<222> LOCATION: (125)...(125)		
273	<223> OTHER INFORMATION: unknown		
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276	<222> LOCATION: (128)...(128)		
277	<223> OTHER INFORMATION: unknown		
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280	<222> LOCATION: (130)...(130)		
281	<223> OTHER INFORMATION: unknown		
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284	<222> LOCATION: (220)...(220)		
285	<223> OTHER INFORMATION: unknown		
287	<221> NAME/KEY: unsure		
288	<222> LOCATION: (389)...(389)		
289	<223> OTHER INFORMATION: unknown		
291	<221> NAME/KEY: unsure		
292	<222> LOCATION: (409)...(409)		
293	<223> OTHER INFORMATION: unknown		
295	<400> SEQUENCE: 4		
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W--> 297	ccttgcacg caccatctggg tgcctggcc	ttcagcgggn agngngtctt ggggtccag	120
W--> 298	cgcangangn gggagttccc ctttaggat	ctcaatttcg gctggccatt tctgggttc	180
W--> 299	ctggggggca gatctggccg tggggcaat	ggaggagccn aaagggcac ctgcccagc	240
300	tccaaacctcc tgccttcctg gtcactgt	ttccctgtat ctcagcagt agctgaccg	300
301	tagaactgtt agatactcac ggcctccca	gcttgatct cgcagcggca gaaggaaac	360

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/434,708

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Input Set : A:\B8017159.txt  
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L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6